

CRF Errors Corrected by the STIC System Branch

0420 018
 CRF Processing Date: 4/23/02
 Edited by: DC
 Verified by: DC (STIC staff)

Serial Number: 09/921,650c

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: **ENTERED**
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☒ Other: Aligned amino acid numbers in Seq. 2.

***Examiner:** The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.



OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/921,650C

DATE: 04/23/2002
 TIME: 16:08:26

Input Set : A:\PTO.DC.TXT
 Output Set: N:\CRF3\04232002\I921650C.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:
 5 (i) APPLICANT: Bujard, Hermann
 6 Gossen, Manfred
 8 (ii) TITLE OF INVENTION: Tetracycline-Inducible Transcriptional
 9 Inhibitor Fusion Proteins
 11 (iii) NUMBER OF SEQUENCES: 37
 13 (iv) CORRESPONDENCE ADDRESS:
 14 (A) ADDRESSEE: LAHIVE & COCKFIELD
 15 (B) STREET: 28 State Street
 16 (C) CITY: Boston
 17 (D) STATE: Massachusetts
 18 (E) COUNTRY: USA
 19 (F) ZIP: 02109-1875
 21 (v) COMPUTER READABLE FORM:
 22 (A) MEDIUM TYPE: Floppy disk
 23 (B) COMPUTER: IBM PC compatible
 24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 25 (D) SOFTWARE: ASCII Text
 27 (vi) CURRENT APPLICATION DATA:
 C--> 28 (A) APPLICATION NUMBER: US/09/921,650C
 C--> 29 (B) FILING DATE: 31-Aug-2001
 75 (C) CLASSIFICATION:
 C--> 72 (vii) PRIOR APPLICATION DATA:
 33 (A) APPLICATION NUMBER: US 09/489,777
 34 (B) FILING DATE: 24-JAN-2000
 38 (A) APPLICATION NUMBER: US 09/162,184
 39 (B) FILING DATE: 28-SEP-1998
 43 (A) APPLICATION NUMBER: US 08/485,978
 44 (B) FILING DATE: 07-JUN-1995
 48 (A) APPLICATION NUMBER: US 08/383,754
 49 (B) FILING DATE: 03-FEB-1995
 53 (A) APPLICATION NUMBER: US 08/275,876
 54 (B) FILING DATE: 15-JULY-1994
 58 (A) APPLICATION NUMBER: US 08/270,637
 59 (B) FILING DATE: 01-JULY-1994
 63 (A) APPLICATION NUMBER: US 08/260,452
 64 (B) FILING DATE: 14-JUNE-1994
 68 (A) APPLICATION NUMBER: US 08/076,327
 69 (B) FILING DATE: 14-JUNE-1993
 73 (A) APPLICATION NUMBER: US 08/076,726
 74 (B) FILING DATE: 14-JUNE-1993
 77 (viii) ATTORNEY/AGENT INFORMATION:

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/921,650C

DATE: 04/23/2002

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Input Set : A:\PTO.DC.TXT

Output Set: N:\CRF3\04232002\I921650C.raw

78 (A) NAME: DeConti, Giulio A. Jr.
79 (B) REGISTRATION NUMBER: 31,503
80 (C) REFERENCE/DOCKET NUMBER: BBI-009C6CNDVCN
82 (ix) TELECOMMUNICATION INFORMATION:
83 (A) TELEPHONE: (617)227-7400
84 (B) TELEFAX: (617)742-4214
86 (2) INFORMATION FOR SEQ ID NO: 1:
88 (i) SEQUENCE CHARACTERISTICS:
89 (A) LENGTH: 1008 base pairs
90 (B) TYPE: nucleic acid
91 (C) STRANDEDNESS: double
92 (D) TOPOLOGY: linear
W--> 94 (ii) MOLECULE TYPE: DNA
96 (ix) FEATURE:
97 (A) NAME/KEY: exon
98 (B) LOCATION: 1..1008
100 (ix) FEATURE:
101 (A) NAME/KEY: mRNA
102 (B) LOCATION: 1..1008
104 (ix) FEATURE:
105 (A) NAME/KEY: misc. binding
106 (B) LOCATION: 1..207
108 (ix) FEATURE:
109 (A) NAME/KEY: misc. binding
110 (B) LOCATION: 208..335
112 (ix) FEATURE:
113 (A) NAME/KEY: CDS
114 (B) LOCATION: 1..1005
116 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
118 ATG TCT AGA TTA GAT AAA AGT AAA GTG ATT AAC AGC GCA TTA GAG CTG 48
119 Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu
120 1 5 10 15
122 CTT AAT GAG GTC GGA ATC GAA GGT TTA ACA ACC CGT AAA CTC GCC CAG 96
123 Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln
124 20 25 30
126 AAG CTA GGT GTA GAG CAG CCT ACA CTG TAT TGG CAT GTA AAA AAT AAG 144
127 Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys
128 35 40 45
130 CGG GCT TTG CTC GAC GCC TTA GCC ATT GAG ATG TTA GAT AGG CAC CAT 192
131 Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His
132 50 55 60
134 ACT CAC TTT TGC CCT TTA AAA GGG GAA AGC TGG CAA GAT TTT TTA CGC 240
135 Thr His Phe Cys Pro Leu Lys Gly Glu Ser Trp Gln Asp Phe Leu Arg
136 65 70 75 80
138 AAT AAG GCT AAA AGT TTT AGA TGT GCT TTA CTA AGT CAT CGC AAT GGA 288
139 Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asn Gly
140 85 90 95
142 GCA AAA GTA CAT TCA GAT ACA CGG CCT ACA GAA AAA CAG TAT GAA ACT 336
143 Ala Lys Val His Ser Asp Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr

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144		100		105		110		
146	CTC	GAA	AAT	CAA	TTA	GCC	TTT	TTA
147	Leu	Glu	Asn	Gln	Leu	Ala	Phe	Leu
148			115			120		125
150	AAT	GCA	TTA	TAT	GCA	CTC	AGC	GCT
151	Asn	Ala	Leu	Tyr	Ala	Leu	Ser	Ala
152		130				135		140
154	GTA	TTG	GAA	GAT	CAA	GAG	CAT	CAA
155	Val	Leu	Glu	Asp	Gln	His	Gln	Val
156	145					150		155
158	CCT	ACT	ACT	GAT	AGT	ATG	CCG	CCA
159	Pro	Thr	Thr	Asp	Ser	Met	Pro	Pro
160				165				170
162	TTT	GAT	CAC	CAA	GGT	GCA	GAG	CCA
163	Phe	Asp	His	Gln	Gly	Ala	Glu	Pro
164			180					185
166	ATC	ATA	TGC	GGA	TTA	GAA	AAA	CAA
167	Ile	Ile	Cys	Gly	Leu	Glu	Lys	Gln
168			195					200
170	TAC	AGC	CGC	GCG	CGT	ACG	AAA	AAC
171	Tyr	Ser	Arg	Ala	Arg	Thr	Lys	Asn
172		210						215
174	CTG	CTC	GAT	CTC	CCG	GAC	GAC	GAC
175	Leu	Leu	Asp	Leu	Pro	Asp	Asp	Asp
176	225					230		235
178	GCT	CCG	CGC	CTG	TCC	TTT	CTC	CCC
179	Ala	Pro	Arg	Leu	Ser	Phe	Leu	Pro
180				245				250
182	ACG	GCC	CCC	CCG	ACC	GAT	GTC	AGC
183	Thr	Ala	Pro	Pro	Thr	Asp	Val	Ser
184			260					265
186	GGC	GAG	GAC	GTG	GCG	ATG	GCG	CAT
187	Gly	Glu	Asp	Val	Ala	Met	Ala	His
188			275					280
190	CTG	GAC	ATG	TTG	GGG	GAC	GGG	GAT
191	Leu	Asp	Met	Leu	Gly	Asp	Gly	Asp
192		290						295
194	CAC	GAC	TCC	GCC	CCC	TAC	GGC	GCT
195	His	Asp	Ser	Ala	Pro	Tyr	Gly	Ala
196	305					310		315
198	GAG	CAG	ATG	TTT	ACC	GAT	CCC	CTT
199	Glu	Gln	Met	Phe	Thr	Asp	Pro	Leu
200				325				330
202	(2)	INFORMATION FOR SEQ ID NO: 2:						
204	(i)	SEQUENCE CHARACTERISTICS:						
205		(A)	LENGTH: 335 amino acids					
206		(B)	TYPE: amino acid					
207		(D)	TOPOLOGY: linear					
209	(ii)	MOLECULE TYPE: protein						

RAW SEQUENCE LISTING

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TIME: 16:08:26

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Output Set: N:\CRF3\04232002\I921650C.raw

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211      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
213 Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu
214   1          5          10          15
216 Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln
217          20          25          30
219 Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys
220          35          40          45
222 Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His
223          50          55          60
225 Thr His Phe Cys Pro Leu Lys Gly Glu Ser Trp Gln Asp Phe Leu Arg
226   65          70          75          80
228 Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asn Gly
229          85          90          95
231 Ala Lys Val His Ser Asp Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr
232          100          105          110
234 Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu
235          115          120          125
237 Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys
238          130          135          140
240 Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr
241  145          150          155          160
243 Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu
244          165          170          175
246 Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu
247          180          185          190
249 Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser Ala
250          195          200          205
252 Tyr Ser Arg Ala Arg Thr Lys Asn Asn Tyr Gly Ser Thr Ile Glu Gly
253          210          215          220
255 Leu Leu Asp Leu Pro Asp Asp Asp Ala Pro Glu Glu Ala Gly Leu Ala
256  225          230          235          240
258 Ala Pro Arg Leu Ser Phe Leu Pro Ala Gly His Thr Arg Arg Leu Ser
259          245          250          255
261 Thr Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp
262          260          265          270
264 Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
265          275          280          285
267 Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
268          290          295          300
270 His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
271  305          310          315          320
273 Glu Gln Met Phe Thr Asp Pro Leu Gly Ile Asp Glu Tyr Gly Gly
274          325          330          335

```

277 (2) INFORMATION FOR SEQ ID NO: 3:

279 (i) SEQUENCE CHARACTERISTICS:

280 (A) LENGTH: 33 base pairs

281 (B) TYPE: nucleic acid

282 (C) STRANDEDNESS: double

283 (D) TOPOLOGY: linear

RAW SEQUENCE LISTING

DATE: 04/23/2002

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TIME: 16:08:26

Input Set : A:\PTO.DC.TXT

Output Set: N:\CRF3\04232002\I921650C.raw

```

W--> 285      (ii) MOLECULE TYPE: DNA
288      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
290 GAC GCG CTA GAC GAT TTC GAT CTG GAC ATG TTG      33
291 Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu
292 1      5      10
295 (2) INFORMATION FOR SEQ ID NO: 4:
297      (i) SEQUENCE CHARACTERISTICS:
298          (A) LENGTH: 11 amino acids
299          (B) TYPE: amino acid
300          (D) TOPOLOGY: linear
302      (ii) MOLECULE TYPE: peptide
304      (v) FRAGMENT TYPE: internal
307      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
309      Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu
310      1      5      10
313 (2) INFORMATION FOR SEQ ID NO: 5:
315      (i) SEQUENCE CHARACTERISTICS:
316          (A) LENGTH: 7 amino acids
317          (B) TYPE: amino acid
318          (D) TOPOLOGY: linear
320      (ii) MOLECULE TYPE: peptide
322      (v) FRAGMENT TYPE: internal
325      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
327      Met Pro Lys Arg Pro Arg Pro
328      1      5
331 (2) INFORMATION FOR SEQ ID NO: 6:
333      (i) SEQUENCE CHARACTERISTICS:
334          (A) LENGTH: 569 base pairs
335          (B) TYPE: nucleic acid
336          (C) STRANDEDNESS: double
337          (D) TOPOLOGY: linear
W--> 339      (ii) MOLECULE TYPE: DNA
342      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
344 GAATTCGGGG CCGCGGAGGC TGGATCGGTC CCGGTGTCTT CTATGGAGGT CAAAACAGCG      60
346 TGGATGGCGT CTCCAGGCCA TCTGACGGTT CACTAAACGA GCTCTGCTTA TATAGGTCGA      120
348 GTTTACCACT CCCTATCAGT GATAGAGAAA AGTGAAAGTC GAGTTTACCA CTCCCTATCA      180
350 GTGATAGAGA AAAGTGAAAG TCGAGTTTAC CACTCCCTAT CAGTGATAGA GAAAAGTGAA      240
352 AGTCGAGTTT ACCACTCCCT ACCAGTGATA GAGAAAAGTG AAAGTCGAGT TTACCACTCC      300
354 CTATCAGTGA TAGAGAAAAG TGAAAGTCGA GTTTACCACT CCCTATCAGT GATAGAGAAA      360
356 AGTGAAAGTC GAGTTTACCA CTCCCTATCA GTGATAGAGA AAAGTGAAAG TCGAGCTCGG      420
358 TACCCGGGTC GAGTAGGCGT GTACGGTGGG AGGCCTATAT AAGCAGAGCT CGTTTAGTGA      480
360 ACCGTCAGAT CGCCTGGAGA CGCCATCCAC GCTGTTTTGA CCTCCATAGA AGACACCGGG      540
362 ACCGATCCAG CCTCCGCGGC CCCGAATTC      569
365 (2) INFORMATION FOR SEQ ID NO: 7:
367      (i) SEQUENCE CHARACTERISTICS:
368          (A) LENGTH: 520 base pairs
369          (B) TYPE: nucleic acid
370          (C) STRANDEDNESS: double
371          (D) TOPOLOGY: linear

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/921,650C

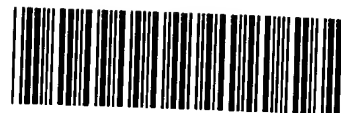
DATE: 04/23/2002

TIME: 16:08:27

Input Set : A:\PTO.DC.TXT

Output Set: N:\CRF3\04232002\I921650C.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:37 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:42 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:47 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:52 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:57 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:62 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:67 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:72 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:94 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1
L:285 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3
L:339 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6
L:373 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7
L:513 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=11
L:529 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=12
L:545 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=13
L:560 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=14
L:576 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=15
L:1028 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=24
L:1044 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=25
L:1078 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=27
L:1438 M:111 C: (47) String data converted to upper case,
M:111 Repeated in SeqNo=35
L:1480 M:111 C: (47) String data converted to upper case,
M:111 Repeated in SeqNo=36
L:1516 M:111 C: (47) String data converted to upper case,
M:111 Repeated in SeqNo=37



Does Not Comply
Corrected Diskette Needed

OIKE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/921,650C

DATE: 04/18/2002
TIME: 14:18:57

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\04182002\I921650C.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Bujard, Hermann
6 Gossen, Manfred

8 (ii) TITLE OF INVENTION: Tetracycline-Inducible Transcriptional
9 Inhibitor Fusion Proteins

11 (iii) NUMBER OF SEQUENCES: 37

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: LAHIVE & COCKFIELD

15 (B) STREET: 28 State Street

16 (C) CITY: Boston

17 (D) STATE: Massachusetts

18 (E) COUNTRY: USA

19 (F) ZIP: 02109-1875

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk

23 (B) COMPUTER: IBM PC compatible

24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

25 (D) SOFTWARE: ASCII Text

27 (vi) CURRENT APPLICATION DATA:

C--> 28 (A) APPLICATION NUMBER: US/09/921,650C

C--> 29 (B) FILING DATE: 31-Aug-2001

75 (C) CLASSIFICATION:

C--> 72 (vii) PRIOR APPLICATION DATA:

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49 (B) FILING DATE: 03-FEB-1995

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59 (B) FILING DATE: 01-JULY-1994

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64 (B) FILING DATE: 14-JUNE-1994

68 (A) APPLICATION NUMBER: US 08/076,327

69 (B) FILING DATE: 14-JUNE-1993

73 (A) APPLICATION NUMBER: US 08/076,726

74 (B) FILING DATE: 14-JUNE-1993

77 (viii) ATTORNEY/AGENT INFORMATION:

RAW SEQUENCE LISTING

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Input Set : A:\Seqlist.txt

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78 (A) NAME: DeConti, Giulio A. Jr.
 79 (B) REGISTRATION NUMBER: 31,503
 80 (C) REFERENCE/DOCKET NUMBER: BBI-009C6CNDVCN
 82 (ix) TELECOMMUNICATION INFORMATION:
 83 (A) TELEPHONE: (617)227-7400
 84 (B) TELEFAX: (617)742-4214

ERRORED SEQUENCES

202 (2) INFORMATION FOR SEQ ID NO: 2:
 204 (i) SEQUENCE CHARACTERISTICS:
 205 (A) LENGTH: 335 amino acids
 206 (B) TYPE: amino acid
 207 (D) TOPOLOGY: linear
 209 (ii) MOLECULE TYPE: protein
 211 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 213 Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu
 214 1 5 10 15
 216 Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln
 217 20 25 30
 219 Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys
 220 35 40 45
 222 Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His
 223 50 55 60
 225 Thr His Phe Cys Pro Leu Lys Gly Glu Ser Trp Gln Asp Phe Leu Arg
 226 65 70 75 80
 228 Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asn Gly
 229 85 90 95
 231 Ala Lys Val His Ser Asp Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr
 232 100 105 110
 234 Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu
 235 115 120 125
 237 Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys
 238 130 135 140
 240 Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr
 241 145 150 155 160
 243 Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu
 244 165 170 175
 246 Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu
 247 180 185 190
 249 Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser Ala
 250 195 200 205
 252 Tyr Ser Arg Ala Arg Thr Lys Asn Asn Tyr Gly Ser Thr Ile Glu Gly
 253 210 215 220
 255 Leu Leu Asp Leu Pro Asp Asp Ala Pro Glu Glu Ala Gly Leu Ala
 256 225 230 235 240
 258 Ala Pro Arg Leu Ser Phe Leu Pro Ala Gly His Thr Arg Arg Leu Ser
 259 245 250 255

RAW SEQUENCE LISTING

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TIME: 14:18:57

Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\04182002\I921650C.raw

261 Thr Ala ^{move over} Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp
 E--> 262 (260) 265 270
 264 Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
 E--> 265 275 280 285
 267 Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
 E--> 268 290 295 300
 270 His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
 E--> 271 305 310 315 320
 273 Glu Gln Met Phe Thr Asp Pro Leu Gly Ile Asp Glu Tyr Gly Gly
 E--> 274 325 330 335

VERIFICATION SUMMARY

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PATENT APPLICATION: US/09/921,650C

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Input Set : A:\Seqlist.txt

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L:67 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:72 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
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L:262 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
M:332 Repeated in SeqNo=2
L:285 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3
L:339 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6
L:373 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7
L:513 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=11
L:529 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=12
L:545 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=13
L:560 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=14
L:576 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=15
L:1028 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=24
L:1044 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=25
L:1078 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=27
L:1438 M:111 C: (47) String data converted to upper case,
M:111 Repeated in SeqNo=35
L:1480 M:111 C: (47) String data converted to upper case,
M:111 Repeated in SeqNo=36
L:1516 M:111 C: (47) String data converted to upper case,
M:111 Repeated in SeqNo=37